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Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
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Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
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Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
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Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
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Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
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Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
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Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
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Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
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Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
      165          170          175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
      180          185          190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
      195          200          205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
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Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
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Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
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Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
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Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
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Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
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Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
325 330 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
340 345 350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
355 360 365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
370 375 380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385 390 395 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
405 410 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
420 425 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
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Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
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Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465 470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
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Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
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Val Arg His Arg Trp Lys
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<211> 2070

<212> DNA

<213> Homo sapiens

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 <211> 501
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

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Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp
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Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln
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Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
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<212> PRT
<213> Homo sapiens

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<210> 8
<211> 501
<212> PRT
<213> Mus musculus
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Leu Pro Ala Gln Gly Thr His Leu Gly Ile Arg Leu Pro Leu Arg Ser
              20              25              30

Gly Leu Ala Gly Pro Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
              35              40              45

Glu Glu Ser Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
  50              55              60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
  65              70              75              80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
              85              90              95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
              100              105              110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
              115              120              125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
  130              135              140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
  145              150              155              160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
              165              170              175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
              180              185              190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro
  195              200              205

Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
  210              215              220

Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
  225              230              235              240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
              245              250              255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
              260              265              270

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Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
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Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
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<210> 9
<211> 2088
<212> DNA
<213> Homo sapiens

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc aggacacaaa 180
acctgcattg ataccaagga aggcattcctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtgaacca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagtgtgt 360
gagtttgtaa gtgatgccct tctcgttcct gacaagtga aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtga 480
aagagtacca acttgcattga ctacggcatg ttgctgccct gcggaattga caagttccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600

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gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
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gacaagtatc tcgagacacc tggggatgag aatgaacatg cccattttcca gaaagccaaa 960
gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020
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atcgatcatc ctttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
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ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag 2088

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<210> 10
 <211> 695
 <212> PRT
 <213> Homo sapiens

<400> 10
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 35 40 45
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile		
				165					170					175			
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu		
			180					185					190				
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val		
		195					200					205					
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys		
	210					215					220						
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu		
225					230					235					240		
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu		
				245					250					255			
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile		
			260					265					270				
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg		
		275					280					285					
Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu		
	290					295					300						
Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys		
305					310				315					320			
Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg		
				325					330					335			
Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp		
		340						345					350				
Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu		
		355					360					365					
Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala		
	370					375					380						
Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn		
385					390				395						400		
Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe		
			405					410					415				
Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His		
		420					425					430					
Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala		
		435					440				445						
Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu		
	450					455					460						
Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala		
465					470				475					480			
Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn		
				485					490					495			

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

<210> 11
<211> 2088
<212> DNA
<213> Homo sapiens

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180
acctgcattg ataccaagga aggcacctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtacca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccaccccccac tttgtgattc cctaccgctg cttagttggt 360
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<210> 12
<211> 695
<212> PRT
<213> Homo sapiens
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
		195					200					205			
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
	210					215					220				
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
225					230					235					240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
				245					250					255	
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
			260					265					270		
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
		275					280					285			
Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu
	290					295					300				
Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys
305					310					315					320
Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg
				325					330					335	
Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp
			340					345					350		
Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu
		355					360					365			
Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala
	370					375					380				
Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn
385					390					395					400
Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe
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Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His
			420					425					430		
Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala
		435					440					445			
Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu
	450					455					460				
Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala
465					470					475					480
Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn
				485					490					495	
Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser
			500					505					510		

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

<210> 13
<211> 2088
<212> DNA
<213> Homo sapiens

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caggagaaag tggaaatctt ggaacaggaa gcagccaacg agagacagca gctggtggag 1140
acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaa 1200

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<210> 14
<211> 695
<212> PRT
<213> Homo sapiens
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<400> 14															
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Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro
			20					25					30		
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln
		35					40					45			
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp
	50					55					60				
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu
65					70					75					80
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn
				85					90					95	
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val
			100					105					110		
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu
		115					120					125			
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
		130				135					140				
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
145					150					155					160
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
				165					170					175	
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
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Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
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Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
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Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
225					230					235					240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
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Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
			260					265					270		
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
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Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu
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Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys
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Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg
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Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp
			340					345					350		
Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu
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Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala
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Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe
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Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His
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Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala
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Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala
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Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn
				485					490					495	
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Val	Glu	Leu	Leu	Pro	Val	Asn	Gly	Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln
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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
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Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
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His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

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<211> 2094

<212> DNA

<213> Homo sapiens

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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
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Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
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Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
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Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
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Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
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Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
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Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	
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Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	
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Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	
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Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	
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Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	
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Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	
						455					460					
Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	
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Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	
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Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	
			500					505					510			
Tyr	Gly	Asn	Asp	Ala	Leu	Met	Pro	Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr	
		515					520					525				
Val	Glu	Leu	Leu	Pro	Val	Asn	Gly	Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln	
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Pro	Trp	His	Ser	Phe	Gly	Ala	Asp	Ser	Val	Pro	Ala	Asn	Thr	Glu	Asn	
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Glu	Val	Glu	Pro	Val	Asp	Ala	Arg	Pro	Ala	Ala	Asp	Arg	Gly	Leu	Thr	
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Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
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His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
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Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
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Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
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Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
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Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
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Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
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Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
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Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
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Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
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35 40 45
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50 55 60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
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Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
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Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
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Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
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Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
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Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220
Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285
Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320
 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335
 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365
 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400
 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415
 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430
 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445
 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460
 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
 485 490 495
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
 500 505 510
 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
 515 520 525
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
 530 535 540
 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
 545 550 555 560
 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
 565 570 575
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
 580 585 590
 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
 595 600 605
 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
 610 615 620
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
 625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 21
<211> 1341
<212> DNA
<213> Homo sapiens

<400> 21
atggctagca tgactggtgg acagcaaattg ggtcgcggat ccacccagca cggcatccgg 60
ctgcccctgc gcagcggcct gggggggcgcc cccctggggc tgcggctgcc ccgggagacc 120
gacgaagagc ccgaggagcc cggccggagg ggcagctttg tggagatggt ggacaacctg 180
aggggcaagt cggggcaggg ctactacgtg gagatgaccg tgggcagccc cccgcagacg 240
ctcaacatcc tgggtggatac aggcagcagt aactttgcag tgggtgctgc cccccacccc 300
ttcctgcatc gctactacca gaggcagctg tccagcacat accgggacct ccggaagggt 360
gtgtatgtgc cctacaccca gggcaagtgg gaaggggagc tgggcaccga cctggtaagc 420
atcccccatg gcccacacgt cactgtgcgt gccaacattg ctgccatcac tgaatcagac 480
aagttcttca tcaacggctc caactgggaa ggcattcctg ggctggccta tgetgagatt 540
gccaggcctg acgactccct ggagcctttc ttgactctc tggtaaagca gaccacggtt 600
cccaacctct tctccctgca cctttgtggt gctggcttcc cctcaacca gtctgaagtg 660
ctggcctctg tcggaggagg catgatcatt ggaggtatcg accactcgct gtacacaggc 720
agtctctggt atacacccat ccggcgggag tggattatg aggtcatcat tgtgcgggtg 780
gagatcaatg gacaggatct gaaaatggac tgcaaggagt acaactatga caagagcatt 840
gtggacagtg gcaccaccaa ccttcgtttg cccaagaaag tgtttgaagc tgcagtcaaa 900
tccatcaagg cagcctcctc cacggagaag ttccctgatg gtttctggct aggagagcag 960
ctggtgtgct ggcaagcagg caccaccctt tggaaacatt tcccagtcac ctactctac 1020
ctaattgggtg aggttaccaa ccagtccttc cgcataacca tccctccgca gcaataacctg 1080
cggccagtgg aagatgtggc cacgtcccaa gacgactgtt acaagtttgc catctcacag 1140
tcatccacgg gcactgttat gggagctgtt atcatggagg gcttctacgt tgtctttgat 1200
cgggcccga aacgaattgg ctttgcgtgc agcgcttgcc atgtgcacga tgagttcagg 1260
acggcagcgg tggaggccc ttttgcacc ttggacatgg aagactgtgg ctacaacatt 1320
ccacagacag atgagtcatg a 1341

<210> 22
<211> 446
<212> PRT
<213> Homo sapiens

<400> 22
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Thr Gln
1 5 10 15
His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu
20 25 30
Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly
35 40 45
Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser
50 55 60

Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr
 65 70 75 80
 Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala
 85 90 95
 Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser
 100 105 110
 Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly
 115 120 125
 Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly
 130 135 140
 Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp
 145 150 155 160
 Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala
 165 170 175
 Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp
 180 185 190
 Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu
 195 200 205
 Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val
 210 215 220
 Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly
 225 230 235 240
 Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile
 245 250 255
 Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys
 260 265 270
 Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu
 275 280 285
 Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala
 290 295 300
 Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln
 305 310 315 320
 Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val
 325 330 335
 Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile
 340 345 350
 Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr
 355 360 365
 Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly
 370 375 380
 Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp
 385 390 395 400

102090-476660

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His
405 410 415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp
420 425 430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
435 440 445

<210> 23
<211> 1380
<212> DNA
<213> Homo sapiens

<400> 23
atggctagca tgactgggtg acagcaaata ggtcgcggat cgatgactat ctctgactct 60
ccgcgtgaac aggacggatc caccagcac ggcacccggc tgcccctgcg cagcggcctg 120
gggggcgccc ccctgggggt ggcgctgccc cgggagaccg acgaagagcc cgaggagccc 180
ggccggaggg gcagctttgt ggagatgggt gacaacctga ggggcaagtc ggggcagggc 240
tactacgtgg agatgaccgt gggcagcccc ccgcagacgc tcaacatcct ggtggataca 300
ggcagcagta actttgcagt ggggtgctgcc cccacccctt tcctgcatcg ctactaccag 360
aggcagctgt ccagcacata ccgggacctc cggaagggtg tgtatgtgcc ctacaccag 420
ggcaagtggg aaggggagct gggcaccgac ctggttaagca tcccccatgg cccaacgtc 480
actgtgcgtg ccaacattgc tgccatcact gaatcagaca agttcttcat caacggctcc 540
aactgggaag gcatacctggg gctggcctat gctgagattg ccaggcctga cgactccctg 600
gagcctttct ttgactctct ggtaaagcag acccacgttc ccaacctctt ctccctgcac 660
ctttgtgggt ctggcttccc cctcaaccag tctgaagtgc tggcctctgt cggagggagc 720
atgatcattg gaggtatcga ccactcgtg tacacaggca gtctctggta tacacccatc 780
cggcgggagt ggtattatga ggtcatcatt gtgcgggtg agatcaatgg acaggatctg 840
aaaatggact gcaaggagta caactatgac aagagcattg tggacagtgg caccaccaac 900
cttcgtttgc ccaagaaagt gtttgaagct gcagtcaaat ccatacaaggc agcctcctcc 960
acggagaagt tccctgatgg tttctggcta ggagagcagc tgggtgtgctg gcaagcaggc 1020
accacccctt ggaacatttt cccagtcac tcactctacc taatgggtga gggtaccaac 1080
cagtccttcc gcataccat ccttcgcgag caatacctgc ggccagtgga agatgtggcc 1140
acgtcccaag acgactgtta caagtttgcc atctcacagt catccacggg cactgttatg 1200
ggagctgtta tcatggaggg cttctacgtt gtctttgac gggcccgaaa acgaattggc 1260
tttgctgtca gcgcttgcca tgtgcacgat gatttcagga cggcagcggg ggaaggccct 1320
tttgtcacct tggacatgga agactgtggc tacaacattc cacagacaga tgagtcatga 1380

<210> 24
<211> 459
<212> PRT
<213> Homo sapiens

<400> 24
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1 5 10 15
Ile Ser Asp Ser Pro Arg Glu Gln Asp Gly Ser Thr Gln His Gly Ile
20 25 30
Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg
35 40 45
Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly
50 55 60
Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly
65 70 75 80
Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile
85 90 95

Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	
			100					105					110			
Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	
		115					120					125				
Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	
	130					135					140					
Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	
145					150					155					160	
Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	
				165					170					175		
Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	
			180					185					190			
Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	
		195					200					205				
Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	His	Leu	Cys	Gly	Ala	
	210					215					220					
Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	
225					230					235					240	
Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	
				245					250					255		
Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	
			260					265					270			
Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	
		275					280					285				
Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	
	290					295					300					
Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	
305					310					315					320	
Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	
				325					330					335		
Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	
			340					345					350			
Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	
		355					360					365				
Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	
						375					380					
Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	
385					390					395					400	
Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	
				405					410					415		
Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	
			420					425					430			

Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
435 440 445

Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
450 455

<210> 25
<211> 1302
<212> DNA
<213> Homo sapiens

<400> 25
atgactcagc atggtattcg tctgccactg cgtagecggtc tgggtggtgc tccactgggt 60
ctgcgtctgc ccgaggagac cgacgaagag ccgaggagc ccggccggag gggcagcttt 120
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 180
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 240
gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 300
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 360
ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 420
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatactg 480
gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 540
ctggtaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 600
cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggtatc 660
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 720
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 780
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 840
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gtccctgat 900
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 960
ttcccagtc tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1020
atccttcgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1080
tacaagtttg ccatctcaca gtcatccacg ggcactgtta tgggagctgt tatcatggag 1140
ggcttctacg ttgtctttga tcggggcccga aaacgaattg gctttgctgt cagcgcttgc 1200
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1260
gaagactgtg gctacaacat tccacagaca gatgagtcat ga 1302

<210> 26
<211> 433
<212> PRT
<213> Homo sapiens

<400> 26
Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly
1 5 10 15
Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu
20 25 30
Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg
35 40 45
Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro
50 55 60
Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala
65 70 75 80
Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln
85 90 95
Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
100 105 110

Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile		
		115					120					125					
Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr		
	130					135					140						
Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu		
145					150					155					160		
Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro		
				165					170					175			
Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser		
			180					185					190				
Leu	His	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu		
		195					200					205					
Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu		
		210				215					220						
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr		
225					230					235					240		
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met		
				245					250					255			
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr		
			260					265					270				
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser		
		275					280					285					
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu		
	290					295					300						
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile		
305					310					315					320		
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser		
				325					330					335			
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp		
			340					345					350				
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser		
		355					360					365					
Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val		
	370					375					380						
Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys		
385					390					395					400		
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val		
				405					410					415			
Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu		
			420					425					430				

Ser

FOUO 4 FEB 96

<210> 27
<211> 1278
<212> DNA
<213> Homo sapiens

<400> 27
atggctagca tgactggtgg acagcaaattg ggtcgcggtat cgatgactat ctctgactct 60
ccgctggact ctggtatcga aaccgacgga tcctttgtgg agatggtgga caacctgagg 120
ggcaagtctg ggagggtgta ctacgtggag atgaccgtgg gcagcccccc gcagacgctc 180
aacatcctgg tggatacagg cagcagtaac tttgcagtgg gtgctgcccc ccacccttc 240
ctgcatcgct actaccagag gcagctgtcc agcacatacc gggacctccg gaagggtgtg 300
tatgtgccct acaccaggg caagtgggaa ggggagctgg gcaccgacct ggtaagcatc 360
ccccatggcc ccaacgtcac tgtgcgtgcc aacattgctg ccatcactga atcagacaag 420
ttcttcatca acggctccaa ctgggaaggc atcctggggc tggcctatgc tgagattgcc 480
aggcctgacg actccctgga gcctttcttt gactctctgg taaagcagac ccacgttccc 540
aacctcttct cctgcacct ttgtggtgct ggcttcccc tcaaccagtc tgaagtgtg 600
gcctctgtcg gagggagcat gatcattgga ggtatcgacc actcgctgta cacaggcagt 660
ctctggtata caccatccg gcgggagtggt tattatgagg tcatcattgt gcgggtggag 720
atcaatggac aggatctgaa aatggactgc aaggagtaca actatgacaa gagcattgtg 780
gacagtggca ccaccaacct tcgtttgccc aagaaagtgt ttgaagctgc agtcaaatac 840
atcaaggcag cctcctccac ggagaagttc cctgatggtt tctggctagg agagcagctg 900
gtgtgctggc aagcaggcac cacccttgg aacattttcc cagtcatttc actctaccta 960
atgggtgagg ttaccaacca gtccttcgcg atcaccatcc ttccgcagca atacctgcgg 1020
ccagtggagg atgtggccac gtcccaagac gactgttaca agtttgcat ctcacagtca 1080
tccacgggca ctgttatggg agctgttata atggagggtc tctacgttgt ctttgatcgg 1140
gcccgaatac gaattggctt tgctgtcagc gcttgccatg tgcacgatga gttcaggacg 1200
gcagcgggtg aaggcccttt tgtcaccttg gacatggaag actgtggcta caacattcca 1260
cagacagatg agtcatga 1278

<210> 28
<211> 425
<212> PRT
<213> Homo sapiens

<400> 28
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1 5 10 15
Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe
20 25 30
Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr
35 40 45
Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val
50 55 60
Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe
65 70 75 80
Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu
85 90 95
Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu
100 105 110
Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val
115 120 125
Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn
130 135 140

Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	145	150	155	160
Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	165	170	175	
Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	His	Leu	Cys	Gly	Ala	Gly	Phe	180	185	190	
Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	195	200	205	
Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	210	215	220	
Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	225	230	235	240
Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	245	250	255	
Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	260	265	270	
Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	275	280	285	
Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	290	295	300	
Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	305	310	315	320
Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	325	330	335	
Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	340	345	350	
Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	355	360	365	
Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	370	375	380	
Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	385	390	395	400
Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	405	410	415	
Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu	Ser								420	425		

<210> 29

<211> 1362

<212> DNA

<213> Homo sapiens

<400> 29

atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgc gctgcccac 60
ggcaccacgc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctgggg 120

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser
450

<210> 31

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 31

atggcccaag ccctgccctg gctcctgctg tggatgggag cgggagtgct gcctgccac 60

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ggcaccacagc acggcatccg gctgcccctg cgcagcggcc tgggggggcgc ccccttgggg 120
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
gtgggtgctg cccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattctg 540
gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
ctggtaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660
cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 720
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 780
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
ttcccagtea tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1080
atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
tacaagtttg ccatctcaca gtcattccac ggcactgtta tgggagctgt tatcatggag 1200
ggcttctacg ttgtctttga tcgggcccga aaacgaattg gctttgctgt cagcgcttgc 1260
catgtgcagc atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
gaagactgtg gctacaacat tccacagaca gatgagtcac agcagcagca gcagcagtga 1380

```

<210> 32

<211> 459

<212> PRT

<213> Homo sapiens

<400> 32

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Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1              5              10              15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
      20              25              30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
      35              40              45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
      50              55              60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
      65              70              75              80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
      85              90              95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
      100             105             110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
      115             120             125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
      130             135             140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
      145             150             155             160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
      165             170             175

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Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp
			180					185					190		
Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro
		195					200					205			
Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln
	210					215					220				
Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile
225					230					235					240
Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg
				245					250					255	
Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln
			260					265					270		
Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val
		275					280					285			
Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala
	290					295					300				
Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp
305					310					315					320
Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr
				325					330					335	
Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val
			340					345					350		
Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg
		355					360					365			
Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala
		370				375					380				
Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu
385					390					395					400
Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala
				405					410					415	
Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu
			420					425					430		
Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro
		435					440					445			
Gln	Thr	Asp	Glu	Ser	His	His	His	His	His	His	His	His	His	His	His
		450				455									

<210> 33
 <211> 25
 <212> PRT
 <213> Homo sapiens

 <400> 33

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<400> 39
cggcatccgg ctgcccctgc gtagcgggtct ggggtgggtget ccactggggtc tgcgtctgcc 60
ccgggagacc gacgaag                                     77
```

<210> 40
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2

<400> 40
cttcgtcggg ctcccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60
ggggcagccg gatgccg 77

<210> 41
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase 8
Cleavage Site

<400> 41
gatcgatgac tatctctgac tctccgctgg actctgggtat cgaaaccgac g 51

<210> 42
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase 8
Cleavage Site

<400> 42
gatccgtcgg ttctgatacc agagtccagc ggagagtcag agatagtcac c 51

<210> 43
<211> 32
<212> DNA
<213> Homo sapiens

<400> 43
aaggatcctt tgtggagatg gtggacaacc tg 32

<210> 44
<211> 36
<212> DNA
<213> Homo sapiens

<400> 44
gaaagctttc atgactcacc tgtctgtgga atgttg 36

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6-His tag

<400> 45
gatcgatca tcaccatcac catg 24

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6-His tag

<400> 46

gatccatggg gatggatg atgc

24

<210> 47

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 47

gactgaccac tcgaccagg tc

22

<210> 48

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 48

cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c

51

<210> 49

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 49

cgaattaaat tccagcacac tggcta

26

<210> 50

<211> 1287

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)
delta TM

<400> 50

atggcccaag ccctgccctg gctcctgctg tggatgggag cgggagtgct gcctgcccac 60
ggcaccacag acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctgggg 120
ctgcggctgc cccgggagac cgacgaagag cccgaggag cggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacctg 540


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<210> 51
<211> 428
<212> PRT
<213> Artificial Sequence
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<400> 51															
Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val
1				5					10					15	
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
			20					25					30		
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
		35					40					45			
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50					55					60				
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65					70					75					80
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
				85					90					95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
			100					105					110		
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
		115					120					125			
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
	130					135					140				
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
145					150					155					160
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp
				165					170					175	
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Leu	Cys	Gly
			180					185					190		
Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly
		195					200					205			

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425

<210> 52

<211> 1305

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)
delta TM

<400> 52

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ggcaccacag acggcatccg gctgccctg cgcagcggcc tggggggcgc cccctgggg 120
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagt ggaaggggag 420
ctgggcaccg acctggtaag catcccccat ggcccacacg tcaactgtgc tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacctctg 540
gggctggcct atgctgagat tgccaggcct tgtggtgctg gcttccccct caaccagtct 600

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gaagtgctgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac 660
acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt catcattgtg 720
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag 780
agcattgtgg acagtggcac caccaacctt cgtttgcccc agaaagtgtt tgaagctgca 840
gtcaaatcca tcaaggcagc ctccctccacg gagaagttcc ctgatggttt ctggctagga 900
gagcagctgg tgtgctggca agcaggcacc accccttgga acattttccc agtcattctca 960
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tacctgcggc cagtgggaaga tgtggccacg tcccaagacg actgttataa gtttgccatc 1080
tcacagtcac ccacgggcac tggttatggga gctgttatca tggagggtt ctacgttgct 1140
tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
ttcaggacgg cagcgggtga aggccctttt gtcaccttgg acatggaaga ctgtggctac 1260
aacattccac agacagatga gtcacagcag cagcagcagc agtga 1305

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<210> 53
 <211> 434
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hu-Asp2(b)
 delta TM

<400> 53
 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15
 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30
 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
 180 185 190
 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His
420 425 430

His His

<210> 54
<211> 2310
<212> DNA
<213> Homo sapiens

<400> 54
atgctgcccg gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggta 60
cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180
acctgcattg ataccaagga aggcacctc cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtgaacca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccaccccccac tttgtgattc cctaccgctg cttagttggg 360
gagtttgtaa gtgatgccct tctcgttcct gacaagtga aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcaactgg cacaccgctc ccaaagagac atgcagtga 480
aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600

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gcggaggagg atgactcgga tgtctggtgg ggccggagcag acacagacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtctgtgg aagaggtggt tgcagaggtg tgctctgaac aagccgagac ggggccgtgc 900
cgagcaatga tctcccgtg gtactttgat gtgactgaag ggaagtgtgc cccattcttt 960
tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg 1020
tgtggcagcg ccatgtccca aagtttactc aagactacc aggaacctct tggccgagat 1080
cctgttaaac ttcctacaac agcagccagt acccctgatg ccgttgacaa gtatctcgag 1140
acacctgggg atgagaatga acatgcccat ttccagaaag ccaaagagag gcttgaggcc 1200
aagcaccgag agagaatgtc ccaggtcatg agagaatggg aagaggcaga acgtcaagca 1260
aagaacttgc cttaaagctga taagaaggca gttatccagc atttccagga gaaagtggaa 1320
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<211> 770

<212> PRT

<213> Homo sapiens

<400> 55

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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
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Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
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Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
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Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
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Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
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Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
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Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
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Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
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Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
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Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
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Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
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Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
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Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
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Gln Asn
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<211> 2253
<212> DNA
<213> Homo sapiens

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<211> 751

<212> PRT

<213> Homo sapiens

<400> 57

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
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Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
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Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
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Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
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Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Ile	Pro	Thr	Thr	Ala	Ala	Ser	Thr
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Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu
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His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	Lys	His	Arg
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Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln
385					390					395					400
Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	Gln	His	Phe
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Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
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Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
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Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
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Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
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Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
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Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
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Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
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Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
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Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
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Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
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Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
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Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
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 <212> DNA
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Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe	
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Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr	
				325					330					335		
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr	
			340					345					350			
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala	
		355					360					365				
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	
	370					375					380					

Glu 385	Asn	Glu	His	Ala	His 390	Phe	Gln	Lys	Ala	Lys 395	Glu	Arg	Leu	Glu	Ala 400
Lys	His	Arg	Glu	Arg 405	Met	Ser	Gln	Val	Met 410	Arg	Glu	Trp	Glu	Glu 415	Ala
Glu	Arg	Gln	Ala 420	Lys	Asn	Leu	Pro	Lys 425	Ala	Asp	Lys	Lys	Ala 430	Val	Ile
Gln	His	Phe 435	Gln	Glu	Lys	Val	Glu 440	Ser	Leu	Glu	Gln	Glu 445	Ala	Ala	Asn
Glu 450	Arg	Gln	Gln	Leu	Val	Glu 455	Thr	His	Met	Ala	Arg 460	Val	Glu	Ala	Met
Leu 465	Asn	Asp	Arg	Arg 470	Arg	Leu	Ala	Leu	Glu 475	Asn	Tyr	Ile	Thr	Ala	Leu 480
Gln	Ala	Val	Pro	Pro 485	Arg	Pro	Arg	His	Val 490	Phe	Asn	Met	Leu	Lys 495	Lys
Tyr	Val	Arg	Ala 500	Glu	Gln	Lys	Asp	Arg 505	Gln	His	Thr	Leu	Lys 510	His	Phe
Glu	His	Val 515	Arg	Met	Val	Asp	Pro 520	Lys	Lys	Ala	Ala	Gln 525	Ile	Arg	Ser
Gln 530	Val	Met	Thr	His	Leu	Arg 535	Val	Ile	Tyr	Glu	Arg 540	Met	Asn	Gln	Ser
Leu 545	Ser	Leu	Leu	Tyr	Asn 550	Val	Pro	Ala	Val	Ala 555	Glu	Glu	Ile	Gln	Asp 560
Glu	Val	Asp	Glu	Leu 565	Leu	Gln	Lys	Glu	Gln 570	Asn	Tyr	Ser	Asp	Asp 575	Val
Leu	Ala	Asn 580	Met	Ile	Ser	Glu	Pro	Arg 585	Ile	Ser	Tyr	Gly	Asn 590	Asp	Ala
Leu	Met	Pro 595	Ser	Leu	Thr	Glu	Thr 600	Lys	Thr	Thr	Val	Glu 605	Leu	Leu	Pro
Val 610	Asn	Gly	Glu	Phe	Ser	Leu 615	Asp	Asp	Leu	Gln 620	Pro	Trp	His	Ser	Phe
Gly 625	Ala	Asp	Ser	Val	Pro 630	Ala	Asn	Thr	Glu	Asn 635	Glu	Val	Glu	Pro	Val 640
Asp	Ala	Arg	Pro	Ala 645	Ala	Asp	Arg	Gly	Leu 650	Thr	Thr	Arg	Pro	Gly 655	Ser
Gly	Leu	Thr	Asn 660	Ile	Lys	Thr	Glu	Glu 665	Ile	Ser	Glu	Val	Lys 670	Met	Asp
Ala	Glu 675	Phe	Arg	His	Asp	Ser	Gly 680	Tyr	Glu	Val	His 685	His	Gln	Lys	Leu
Val 690	Phe	Phe	Ala	Glu	Asp	Val 695	Gly	Ser	Asn	Lys 700	Gly	Ala	Ile	Ile	Gly
Leu 705	Met	Val	Gly	Gly	Val 710	Val	Ile	Ala	Thr	Val 715	Ile	Val	Ile	Thr	Leu 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn Lys Lys
770

<210> 60
<211> 2259
<212> DNA
<213> Homo sapiens

<400> 60
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cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180
acctgcattg ataccaagga aggcattcctg cagtattgcc aagaagtcta cctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtaccca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatcccccac tttgtgattc cctaccgctg cttagt.tgg 360
gagtttgtaa gtgatgccct tctcgttccct gacaagtcca aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtga 480
aagagtacca acttgcata gaacggcatg ttgctgccct gcggaattga caagtccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600
gcggaggagg atgactcgga tgtctggcgg gccggagcag acacagacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtcctgtg aagaggtggt tgcagaggtg tgctctgaac aagccgagac ggggccgtgc 900
cgagcaatga tctcccgtg gtactttgat gtgactgaag ggaagtgtgc cccattcttt 960
tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg 1020
tgtggcagcg ccattcctac aacagcagcc agtaccctg atgccgttga caagtatctc 1080
gagacacctg gggatgagaa tgaacatgcc catttccaga aagccaaaga gaggcttgag 1140
gccaagcacc gagagagaat gtcccaggct atgagagaat ggaagaggc agaacgtcaa 1200
gcaaagaact tgcctaaagc tgataagaag gcagttatcc agcatttcca ggagaaagtg 1260
gaatcttttg aacaggaagc agccaacgag agacagcagc tgggtggagac acacatggcc 1320
agagtggaag ccattgctca tgaccgcccgc cgctggccc tggagaacta catcaccgct 1380
ctgcaggctg ttctcctcgc gcctcgtcac gtgttcaata tgctaaagaa gtatgtccgc 1440
gcagaacaga aggacagaca gcacacccta aagcatttgc agcatgtgcg catggtggat 1500
cccaagaaag ccgctcagat ccggtcccag gttatgacac acctccgtgt gatttatgag 1560
cgcatgaatc agtctctctc cctgctctac aacgtgcctg cagtggccga ggagattcag 1620
gatgaagttg atgagctgct tcagaaagag caaaactatt cagatgacgt cttggccaac 1680
atgattagtg aaccaaggat cagttacgga aacgatgctc tcatgccatc tttgaccgaa 1740
acgaaaacca ccgtggagct ccttcccgtg aatggagagt tcagcctgga cgatctccag 1800
ccgtggcatt cttttggggc tgactctgtg ccagccaaca cagaaaacga agttgagcct 1860
gttgatgccc gccctgctgc cgaccgagga ctgaccactc gaccagggtc tgggttgaca 1920
aatatcaaga cggaggagat ctctgaagtg aagatggatg cagaattccg acatgactca 1980
ggatatgaag ttcatcatca aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa 2040
ggtgcaatca ttggactcat ggtgggcggg gttgtcatag cgacagtgat cgtcatcacc 2100
ttggtgatgc tgaagaagaa acagtacaca tccattcatc atggtgtggt ggaggttgac 2160
gccgctgtca ccccagagga gcgccacctg tccaagatgc agcagaacgg ctacgaaaat 2220
ccaacctaca agttctttga gcagatgcag aacaagaag 2259

<210> 61
<211> 753
<212> PRT
<213> Homo sapiens

<400> 61

Met	Leu	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Ala	Trp	Thr	Ala	Arg
1				5					10					15	
Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro
			20					25					30		
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln
		35					40					45			
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp
	50					55					60				
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu
65					70					75					80
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn
				85					90					95	
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val
			100					105					110		
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu
		115					120					125			
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
	130					135					140				
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
145					150					155					160
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
				165				170						175	
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
			180					185					190		
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
		195					200					205			
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
	210					215					220				
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
225					230					235					240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
				245				250						255	
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
			260					265					270		
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
		275					280					285			
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile
	290					295					300				
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
305					310					315					320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335
 Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
 340 345 350
 Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
 355 360 365
 His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
 370 375 380
 Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
 385 390 395 400
 Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
 405 410 415
 Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
 420 425 430
 Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
 435 440 445
 Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
 450 455 460
 Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
 465 470 475 480
 Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
 485 490 495
 Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
 500 505 510
 Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
 515 520 525
 Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
 530 535 540
 Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
 545 550 555 560
 Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
 565 570 575
 Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
 580 585 590
 Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
 595 600 605
 Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
 610 615 620
 Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
 625 630 635 640
 Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
 645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys
740 745 750

Lys

<210> 62

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 62

Leu Glu Val Leu Phe Gln Gly Pro
1 5

<210> 63

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 63

Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
1 5 10

<210> 64

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 64

Ser Glu Val Lys Met Asp Ala Glu Phe Arg
1 5 10

<210> 65

<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 65
Arg Arg Gly Gly Val Val Ile Ala Thr Val Ile Val Gly Glu Arg
1 5 10 15

<210> 66
<211> 518
<212> PRT
<213> Homo sapiens

<400> 66
Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
1 5 10 15
Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
20 25 30
Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
35 40 45
Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
50 55 60
Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65 70 75 80
Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
85 90 95
Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
100 105 110
Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
115 120 125
Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
130 135 140
Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
145 150 155 160
Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
165 170 175
Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
180 185 190
Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
195 200 205
Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
210 215 220
Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
225 230 235 240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
245 250 255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
260 265 270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
275 280 285

Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
290 295 300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
305 310 315 320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
325 330 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
340 345 350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
355 360 365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
370 375 380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385 390 395 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
405 410 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
420 425 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
435 440 445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
450 455 460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465 470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
485 490 495

Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
500 505 510

Val Arg His Arg Trp Lys
515

<210> 67

<211> 475

<212> PRT

<213> Homo sapiens

<400> 67

Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
1 5 10 15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
 20 25 30
 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
 35 40 45
 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
 50 55 60
 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
 65 70 75 80
 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Glv Tyr Tyr Leu Glu Met
 85 90 95
 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
 100 105 110
 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
 115 120 125
 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
 130 135 140
 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
 145 150 155 160
 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
 165 170 175
 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
 180 185 190
 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
 195 200 205
 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
 210 215 220
 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
 225 230 235 240
 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
 245 250 255
 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
 260 265 270
 Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
 275 280 285
 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
 290 295 300
 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
 305 310 315 320
 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
 325 330 335
 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
 340 345 350

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Asn Ile Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro
165 170 175

Val Ala Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile
180 185 190

Glu Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu
195 200 205

Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln
210 215 220

Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val
225 230 235 240

Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala
245 250 255

Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp
260 265 270

Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr
275 280 285

Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn
290 295 300

Ser Ser Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln
305 310 315 320

Pro Met Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile
325 330 335

Ser Pro Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly
340 345 350

Phe Tyr Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala
355 360 365

Ser Pro Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly
370 375 380

Pro Phe Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser
385 390 395 400

Leu Ser Glu Pro Ile Leu Trp His His His His His His
405 410

<210> 69
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 69
Gly Leu Ala Leu Ala Leu Glu Pro
1 5

<210> 70
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 70
Glu Val Lys Met Asp Ala Glu Phe
1 5

<210> 71
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 71
Glu Val Asn Leu Asp Ala Glu Phe
1 5

<210> 72
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 72
Leu Val Phe Phe Ala Glu Asp Val
1 5

<210> 73
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 73
Lys Leu Val Phe Phe Ala Glu Asp
1 5

<210> 74
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 74
cgctttaagc ttgccaccat gggcgactg gcccgggcg

<210> 75
<211> 57
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 75

cgctttctcg agctaattgt gatggtgatg gtgccacaaa atgggctcgc tcaaaga 57

<210> 76

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<400> 76

Asn Leu Asp Ala

1

<210> 77

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<400> 77

Gly Arg Arg Gly Ser

1

5

<210> 78

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<400> 78

Thr Gln His Gly Ile Arg

1

5

<210> 79

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<400> 79

Glu Thr Asp Glu Glu Pro

1

5

<210> 80

<211> 15

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Peptide

Met Cys Ala Glu Val Lys Met Asp Ala Glu Phe Lys Asp Asn Pro
1 5 10 15

<213> Artificial Sequence

<223> Description of Artificial Sequence: synthetic

Asp Ala Glu Phe Arg
1 5

<213> Artificial Sequence

<223> Description of Artificial Sequence: synthetic

Ser Glu Val Asn Leu
1 5

[illegible]